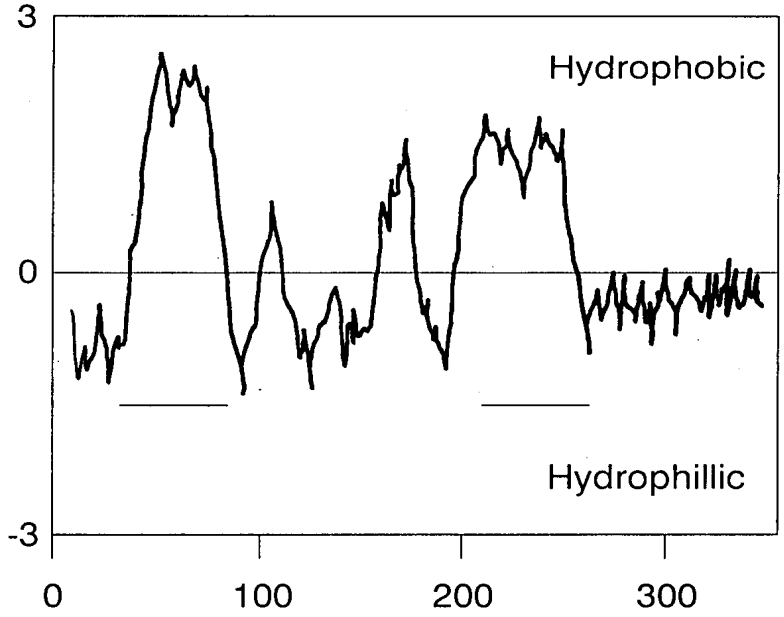


FIGURE 1A

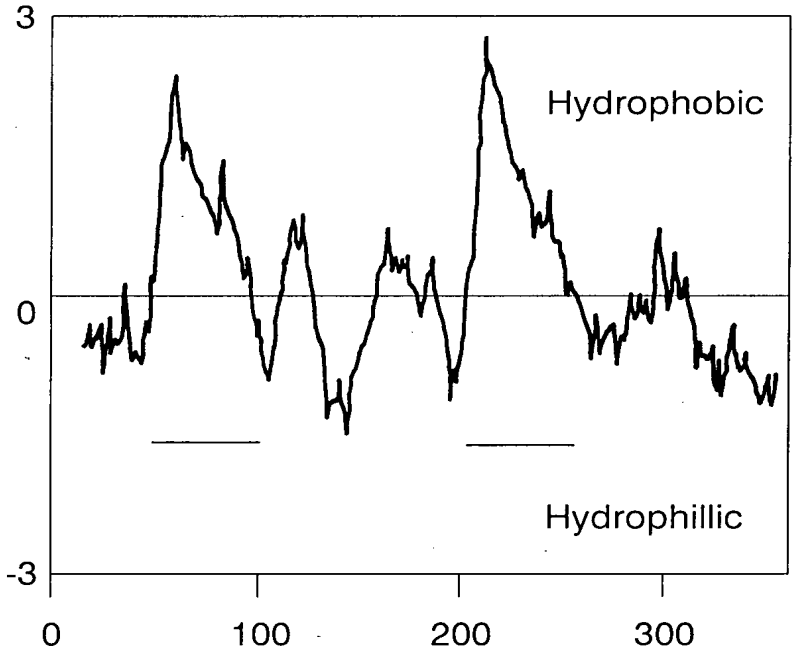


FIGURE 1B

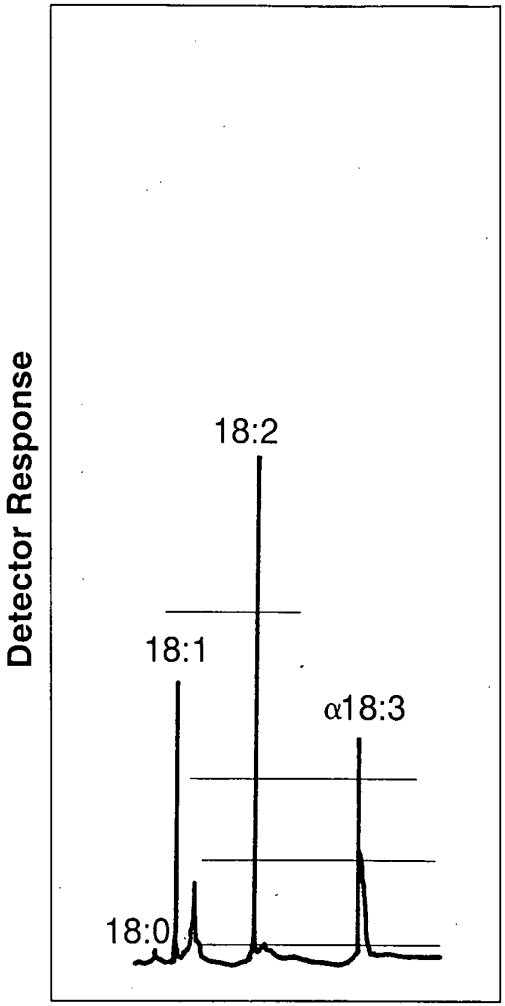


FIGURE 2A

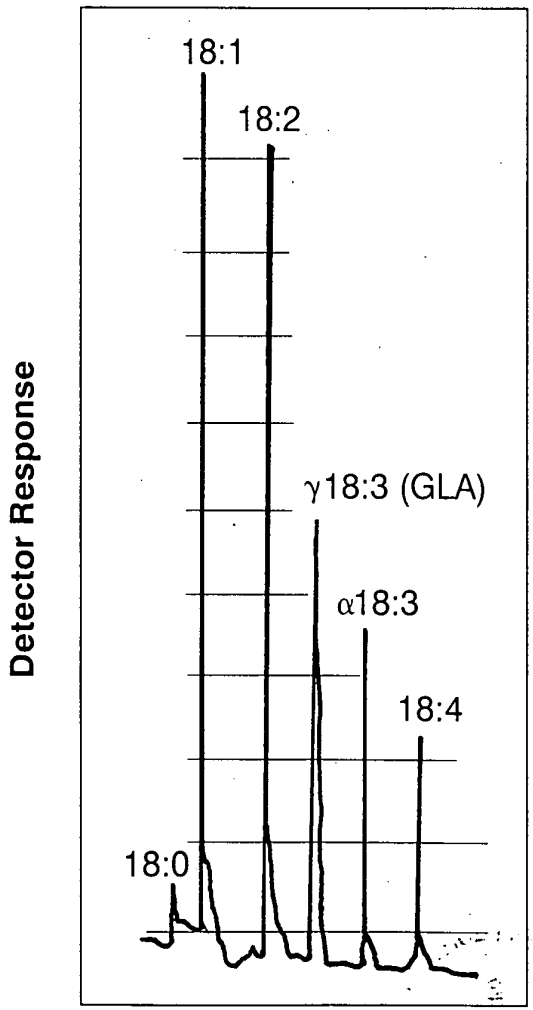


FIGURE 2B

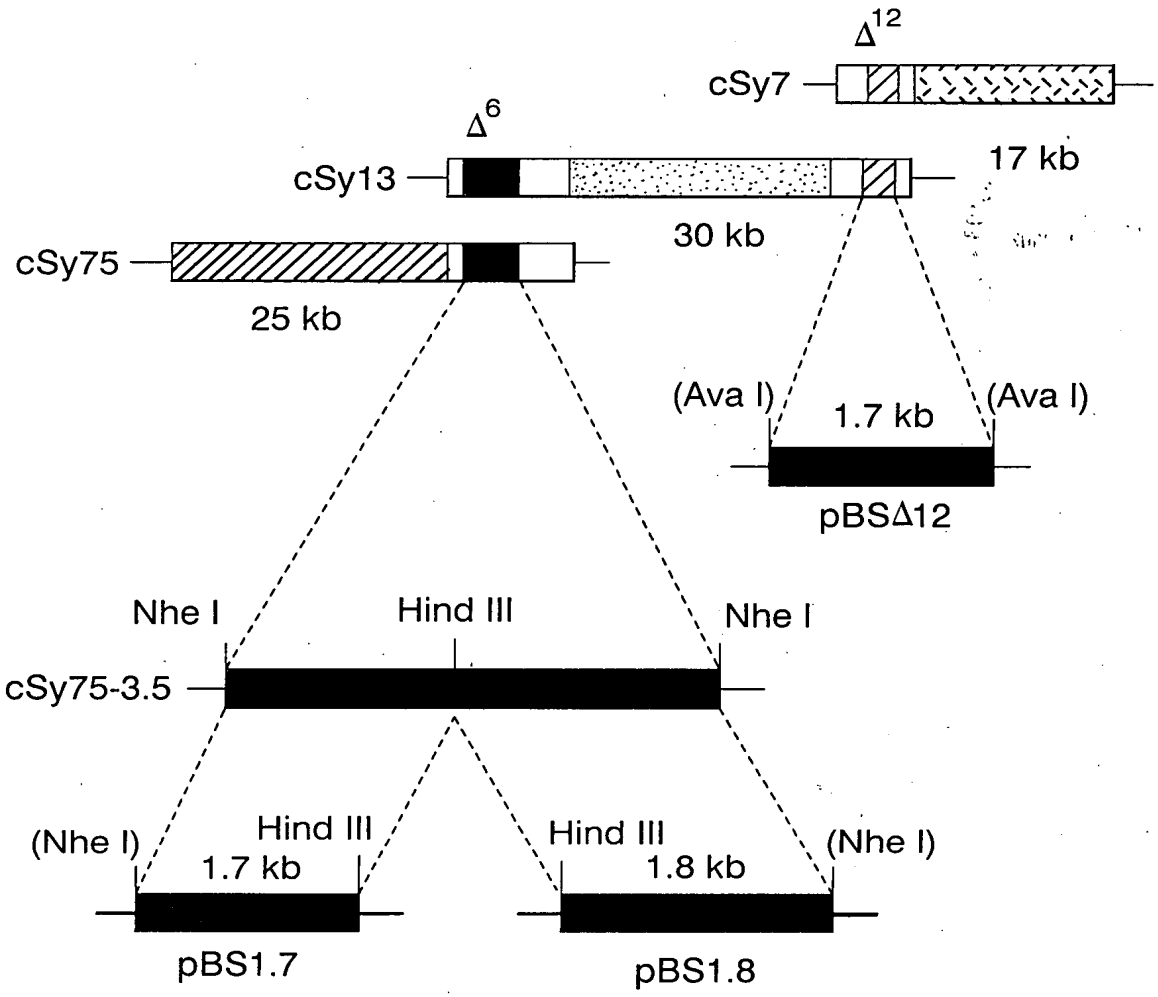

Δ12
cSy7
Δ6
cSy13
17 kb
30 kb
cSy75
25 kb
(Ava I)
1.7 kb
(Ava I)
pBSΔ12
Nhe I
Hind III
Nhe I
cSy75-3.5
(Nhe I)
Hind III
1.7 kb
Hind III
1.8 kb
(Nhe I)
pBS1.7
pBS1.8

FIGURE 3

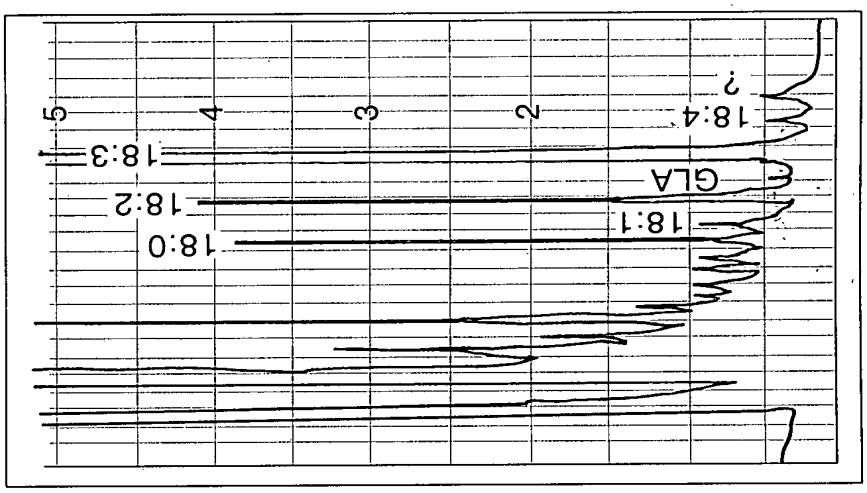


FIGURE 4B

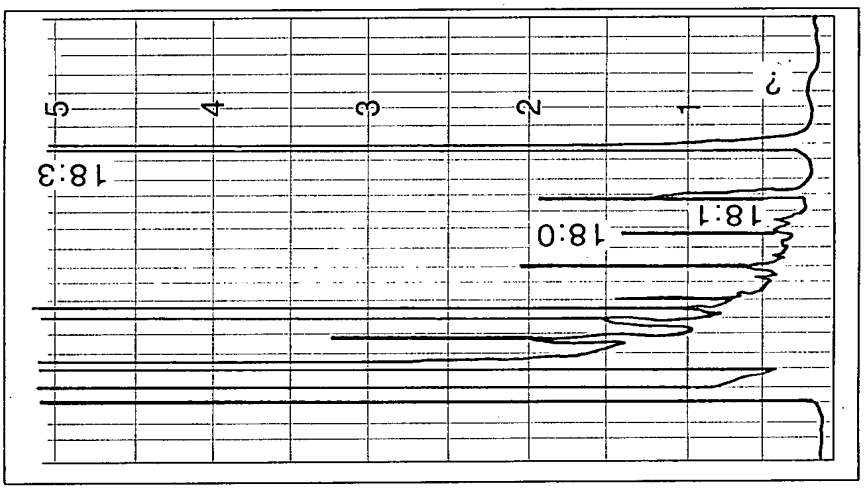


FIGURE 4A

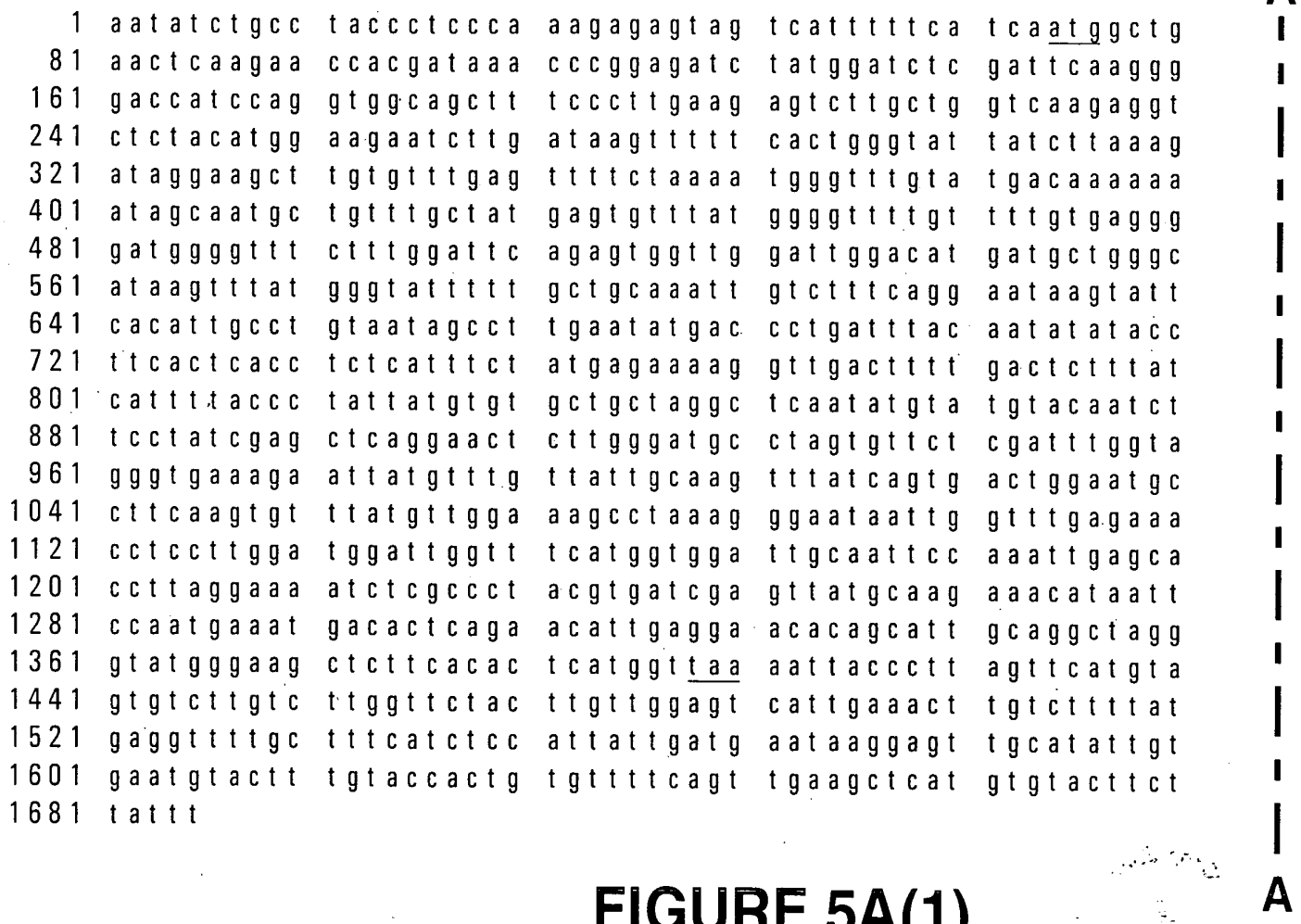

1 aatatctgcc taccctccca aagagagtag tcatttttca tcaatggctg
81 aactcaagaa ccacgataaa cccggagatc tatggatctc gattcaaggg
161 gaccatccag gtggcagctt tcccttgaag agtcttgctg gtcaagaggt
241 ctctacatgg aagaatcttg ataagttttt cactgggtat tatcttaaag
321 ataggaagct tgtgtttgag ttttctaaaa tgggtttgta tgacaaaaaa
401 atagcaatgc tgtttgctat gagtgtttat ggggttttgt tttgtgaggg
481 gatggggttt ctttggattc agagtggttg gattggacat gatgctgggc
561 ataagtttat gggtatttt gctgcaaatt gtctttcagg aataagtatt
641 cacattgcct gtaatagcct tgaatatgac cctgatttac aatatatacc
721 ttcactcacc tctcatttct atgagaaaag gttgacttt gactctttat
801 catttaccc tattatgtgt gctgctaggc tcaatatgta tgtacaatct
881 tcctatcgag ctcaggaact cttgggatgc ctagtgttct cgatttggta
961 gggtgaaaga attatgttt g ttattgcaag tttatcagtg actggaatgc
1041 cttcaagtgt ttatgttgga aagcctaaag ggaataattg gtttgagaaa
1121 cctccttgga tggattggtt tcatggtgga ttgcaattcc aaattgagca
1201 ccttaggaaa atctcgccct acgtgatcga gttatgcaag aaacataatt
1281 ccaatgaaat gacactcaga acattgagga acacagcatt gcaggctagg
1361 gtatgggaag ctcttcacac tcatggttaa aattaccctt agttcatgta
1441 gtgtcttgtc ttggttctac ttgttggagt cattgaaact tgtcttttat
1521 gaggttttgc tttcatctcc attattgatg aataaggagt tgcatattgt
1601 gaatgtactt tgtaccactg tgttttcagt tgaagctcat gtgtacttct
1681 tattt
A
A

FIGURE 5A(1)

A

ctcaaatcaa	gaaatacatt	acctcagatg	80
aaagcctatg	atgtttcgga	ttgggtgaaa	160
aactgatgca	tttgttgcat	tccatcctgc	240
attactctgt	ttctgaggtt	tctaaagatt	320
ggtcatatta	tgtttgcaac	tttgtgcttt	400
tgttttggta	catttgtttt	ctgggtgttt	480
attatatggt	agtgtctgat	tcaaggctta	560
ggttggtgga	aatggaacca	taatgcacat	640
attccttgtt	gtgtcttcca	agtttttttgg	720
caagattctt	tgtaagttat	caacattgga	800
ctcataatgt	tgttgaccaa	gagaaatgtg	880
cccgttgctt	gtttcttgtt	tgcctaattg	960
aacaagttca	gttctccttg	aaccacttct	1040
caaacggatg	ggacacttga	catttcttgt	1120
tcatttgttt	cccaagatgc	ctagatgcaa	1200
tgccttacaa	ttatgcatct	ttctccaagg	1280
gatataacca	agccgctccc	gaagaatttg	1360
ataatttgag	attatgtatc	tcctatgttt	1440
ggtttattag	atgttttttta	atatatttta	1520
caattgttgt	gctcaatatc	tgatattttg	1600
atagactttg	tttaaatggt	tatgtcatgt	1680
			1685

A

FIGURE 5A(2)

```
  1  MAAQI KKYI T  SDELKNHDKP  GDLWI SI QGK  AYDVSDWVKD  HPGGSFPLKS
 81  LKDYSVSEVS  KDYRKLVFEF  SKMGLYDKKG  HI MFATLCFI  AMLFAMSVYG
161  AGHYMVVSDS  RLNKFMGI FA  ANCLSGI SI G  WWKWNHNAHH  I ACNSLEYDP
241  SLSRFFVSYQ  HWTFYPI MCA  ARLNMYVQSL  I MLLTKRNVS  YRAQELLGCL
321  GMQQVQFSLN  HFSSSVYVGK  PKGNNWFEKQ  TDGTLDI SCP  PWMDWFHGGL
401  HNLPYNYASF  SKANEMTLRT  LRNTALQARD  I TKPLPKNLV  WEALHTHG
```

A

A

FIGURE 5B(1)

LAGQEVTDAF	VAFHPASTWK	NLDKFFTGYY	80
VLFCEGVLVH	LFSGCLMGFL	WIQSG**WIGHD**	160
DLQYIPFLVV	SSKFFGSLTS	HFYEKRLTFD	240
VFSIWYPLLV	SCLPNWGERI	MFVIASLSVT	320
QFQIEHHLFP	KMPRCNLRKI	SPYVIELCKK	400
			448

FIGURE 5B(2)

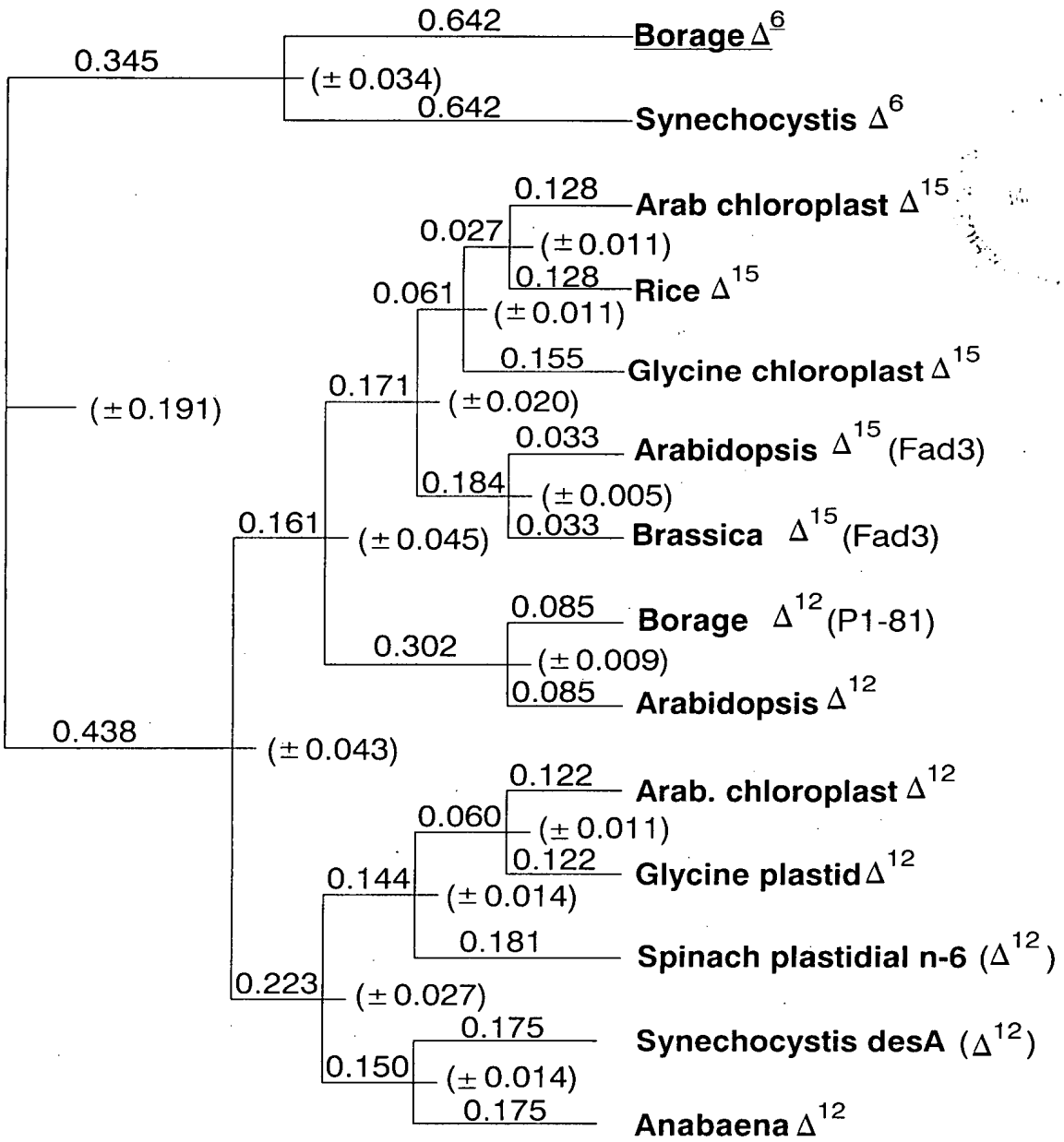

0.642
Borage Δ6
0.345
(±0.034)
0.642
Synechocystis Δ6
0.128
Arab chloroplast Δ15
0.027
(±0.011)
0.128
Rice Δ15
0.061
(±0.011)
0.155
Glycine chloroplast Δ15
0.171
(±0.020)
(±0.191)
0.033
Arabidopsis Δ15 (Fad3)
0.184
(±0.005)
0.161
(±0.045)
0.033
Brassica Δ15 (Fad3)
0.085
Borage Δ12 (P1-81)
0.302
(±0.009)
0.085
Arabidopsis Δ12
0.438
(±0.043)
0.122
Arab. chloroplast Δ12
0.060
(±0.011)
0.122
Glycine plastid Δ12
0.144
(±0.014)
0.181
Spinach plastidial n-6 (Δ12)
0.223
(±0.027)
0.175
Synechocystis desA (Δ12)
0.150
(±0.014)
0.175
Anabaena Δ12

FIGURE 6

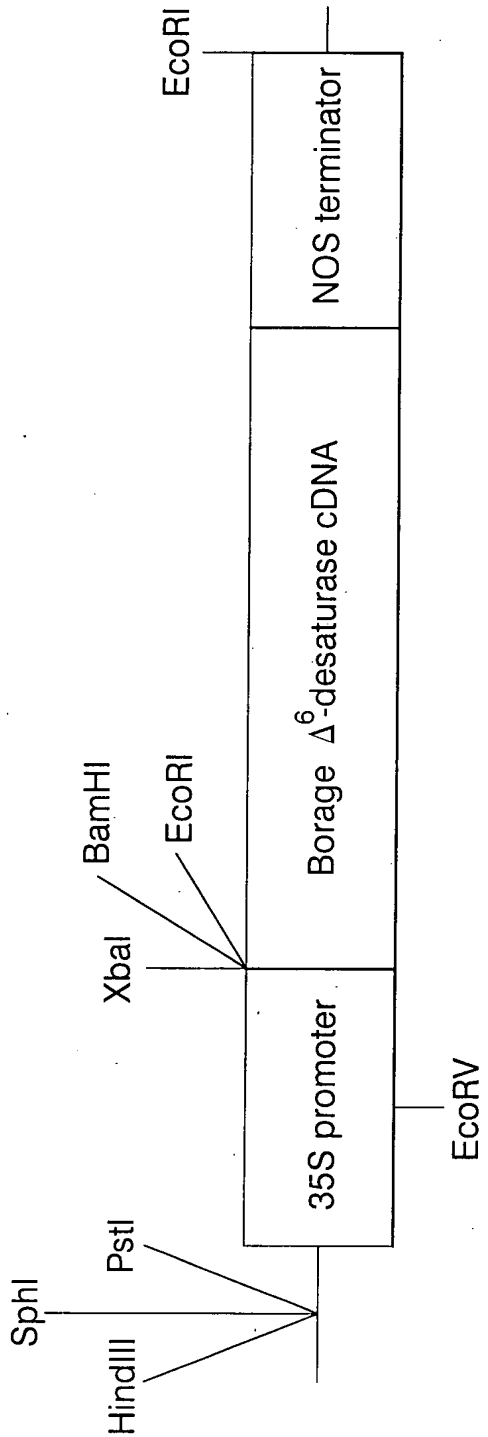

EcoRI
NOS terminator
Borage Δ6-desaturase cDNA
BamHI
EcoRI
XbaI
35S promoter
EcoRV
PstI
SphI
HindIII

FIGURE 7

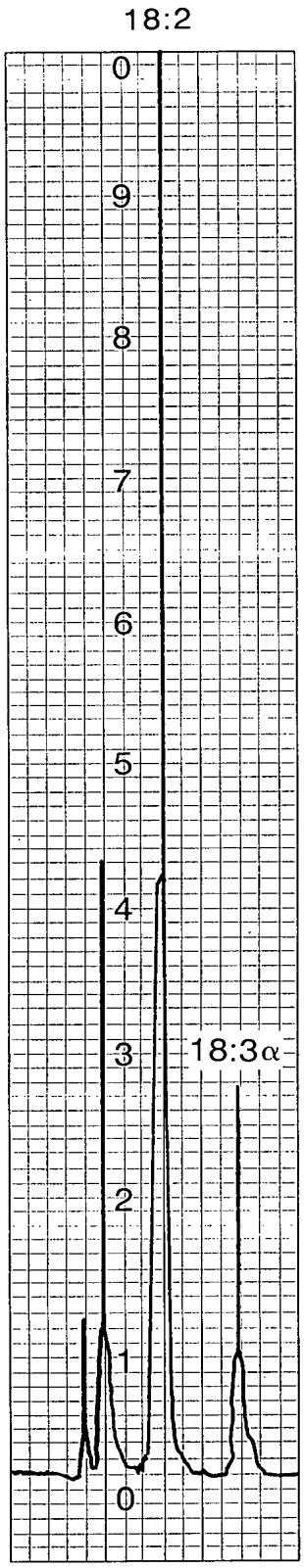


FIGURE 8A

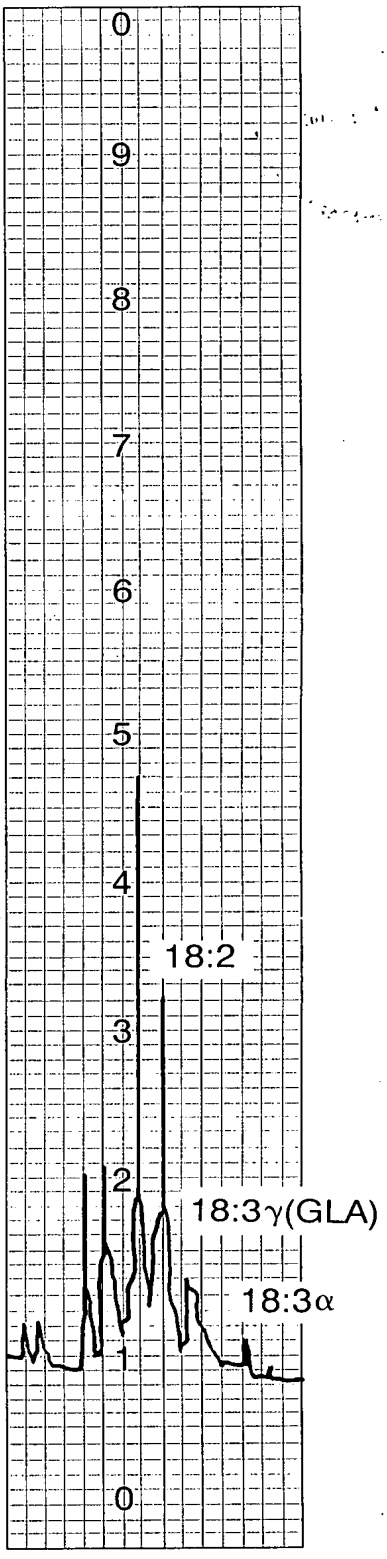


FIGURE 8B

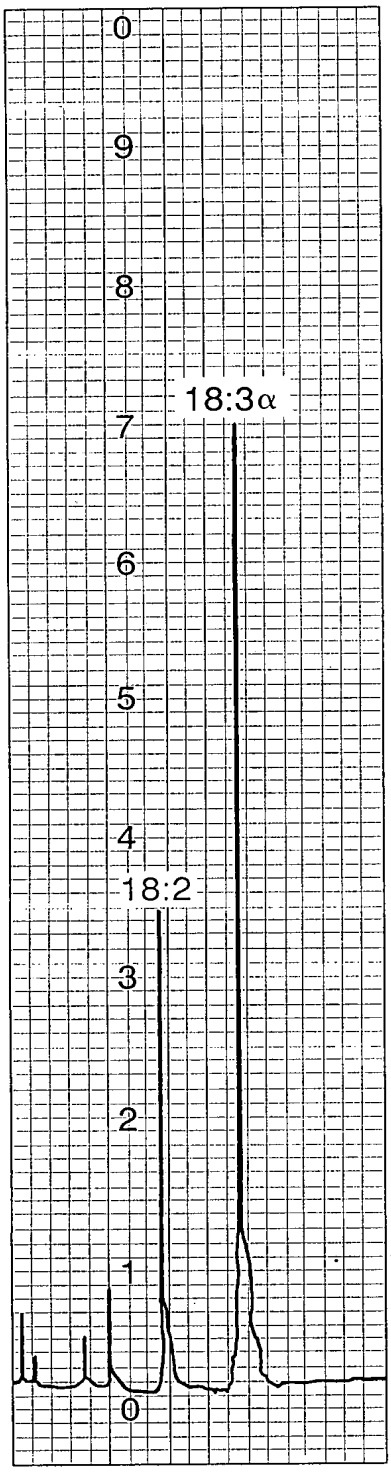


FIGURE 9A

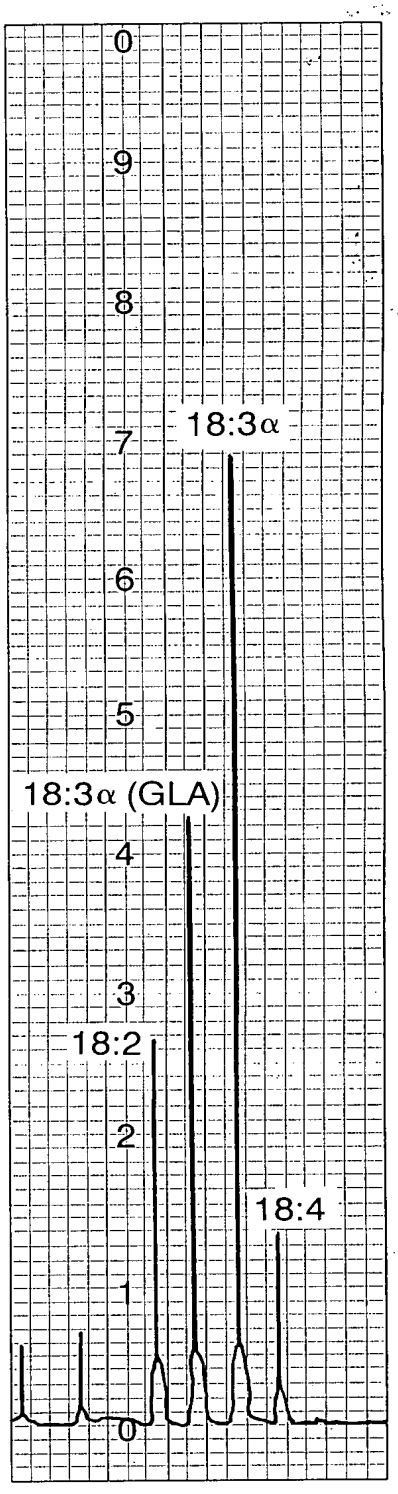


FIGURE 9B

Complete DNA sequence and deduced amino acid sequence of Evening Primrose Putative Δ^6-desaturase

A

CCCCAAAAAATTTTCATTGTTCTCCATCTGGACCACAGCA

GCT AAG AAG TAT ATC ACG GCG GAG GAC CTC CGC CGC CAC AAC
A K K Y I T A E D L R R H N
ATC TCC ATC CAG GGC AAG GTC TAC GAC GTC TCT CGG TGG GCG
I S I Q G K V Y D V S R W A
GAG GTC CCG CTC CTC ATG CTG GCC GGC CAG GAC GTC ACC GAC
E V P L L M L A G Q D V T D
CCG GGC ACG GCG TGG CGG CAT CTG GAT CCG CTC TTC ACC GGC
P G T A W R H L D P L F T G
GAA GTG TCG GAG ATC TCC AAG GAC TAC CGG AGG CTT TTG AAC
E V S E I S K D Y R R L L N
ATC TTC GAG AAG AAG GGC CAC CAC ATC ATG TGG ACG TTC GTC
I F E K K G H H I M W T F V
GCG GCA AtC GTC TAC GGC GTG CTG GCG TCG GAG TCC GTC GGA
A A I V Y G V L A S E S V G
GCA CTG CTG GGC TTG CTG TGG ATC CAA GCC GCG TAT GTG GGC
A L L G L L W I Q A A Y V G

A

B - - - - - - - - - - - - B

FIGURE 10A

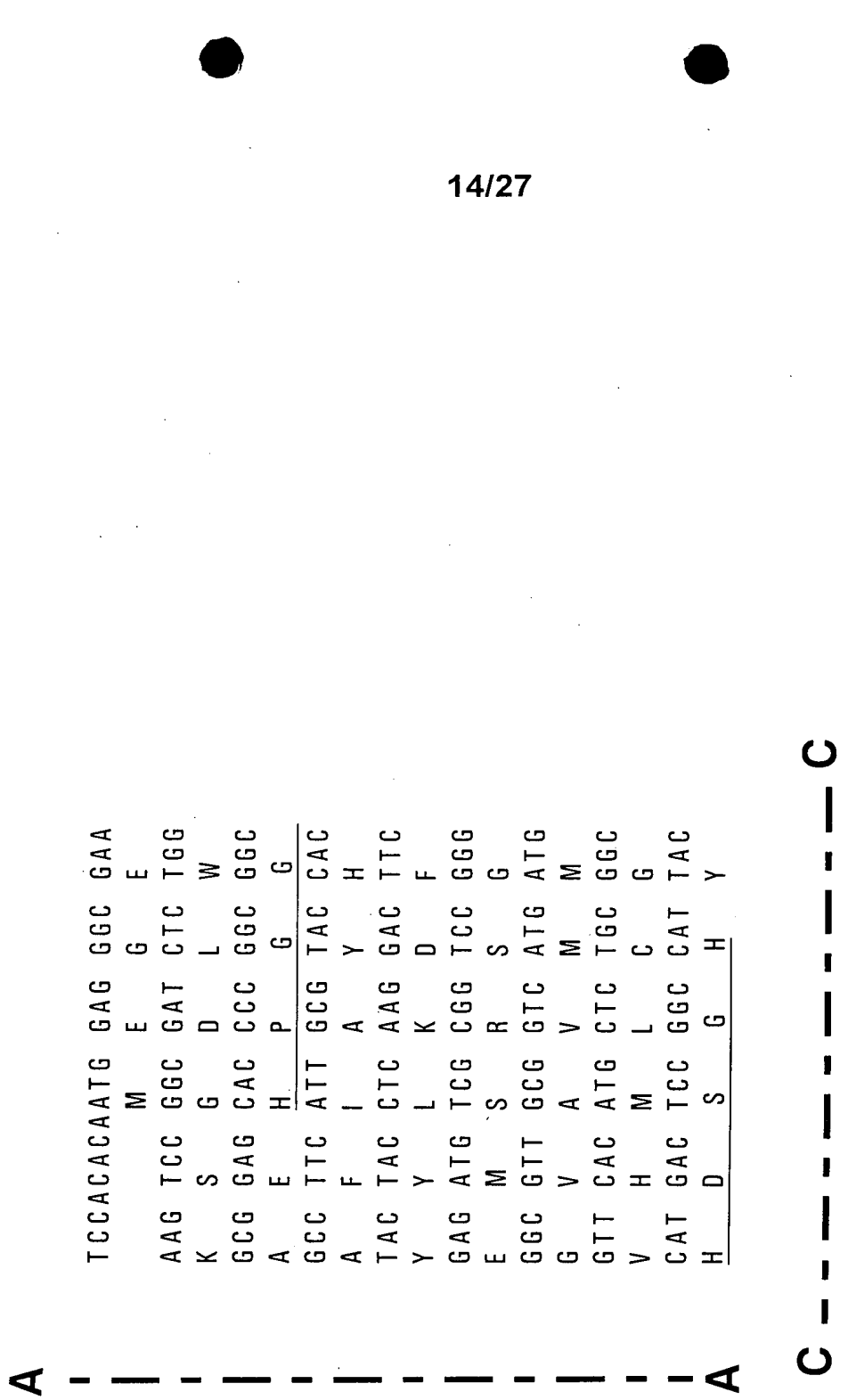

A
TCCACACAATG GAG GGC GAA
M E G E
AAG TCC GGC GAT CTC TGG
K S G D L W
GCG GAG CAC CCC GGC GGC
A E H P G G
GCC TTC ATT GCG TAC CAC
A F I A Y H
TAC TAC CTC AAG GAC TTC
Y Y L K D F
GAG ATG TCG CGG TCC GGG
E M S R S G
GGC GTT GCG GTC ATG ATG
G V A V M M
GTT CAC ATG CTC TGC GGC
V H M L C G
CAT GAC TCC GGC CAT TAC
H D S G H Y
A
C
C

FIGURE 10B

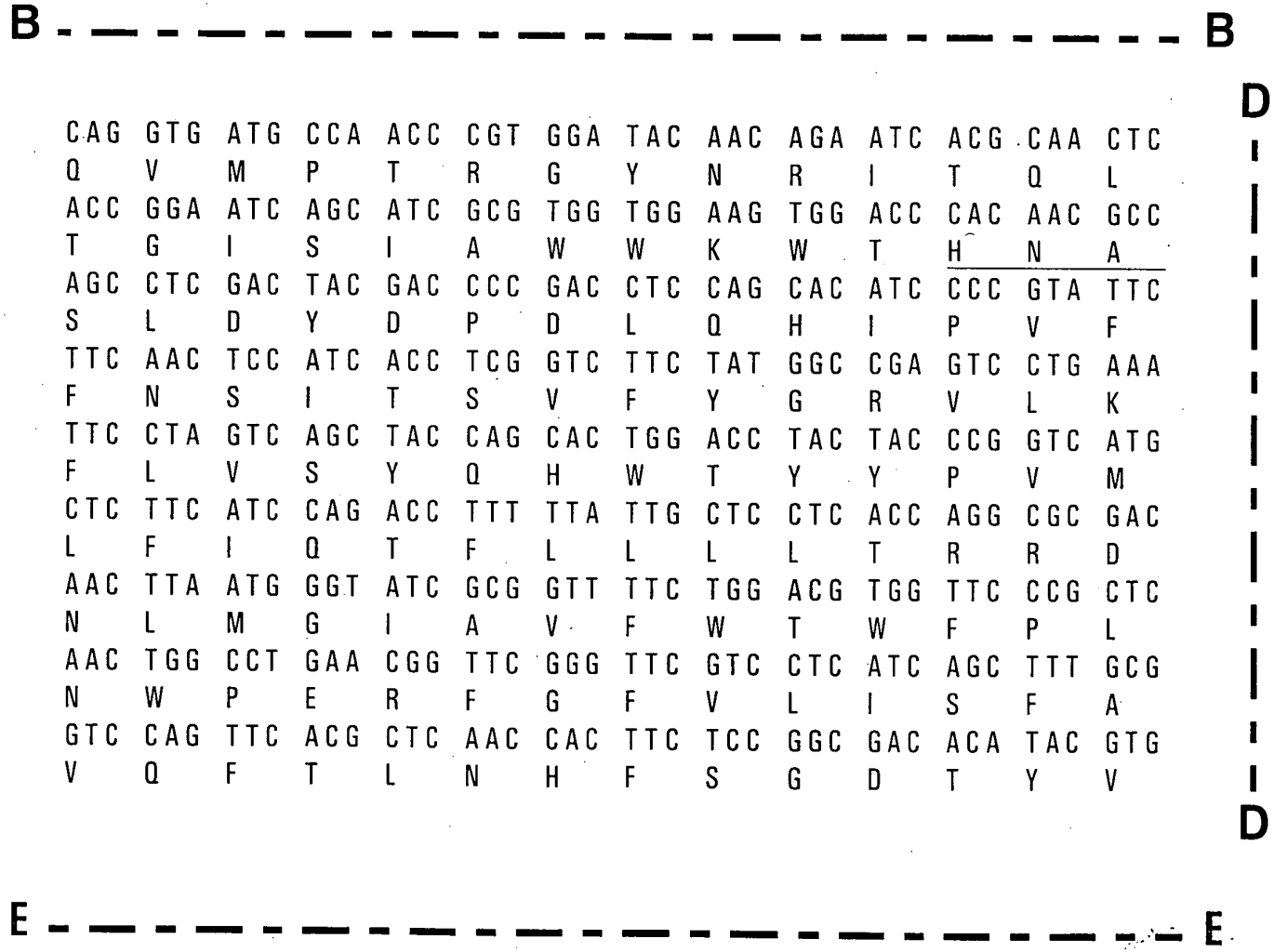

B
B
D
D
E
E
CAG GTG ATG CCA ACC CGT GGA TAC AAC AGA ATC ACG CAA CTC
Q V M P T R G Y N R I T Q L
ACC GGA ATC AGC ATC GCG TGG TGG AAG TGG ACC CAC AAC GCC
T G I S I A W W K W T H N A
AGC CTC GAC TAC GAC CCC GAC CTC CAG CAC ATC CCC GTA TTC
S L D Y D P D L Q H I P V F
TTC AAC TCC ATC ACC TCG GTC TTC TAT GGC CGA GTC CTG AAA
F N S I T S V F Y G R V L K
TTC CTA GTC AGC TAC CAG CAC TGG ACC TAC TAC CCG GTC ATG
F L V S Y Q H W T Y Y P V M
CTC TTC ATC CAG ACC TTT TTA TTG CTC CTC ACC AGG CGC GAC
L F I Q T F L L L L T R R D
AAC TTA ATG GGT ATC GCG GTT TTC TGG ACG TGG TTC CCG CTC
N L M G I A V F W T W F P L
AAC TGG CCT GAA CGG TTC GGG TTC GTC CTC ATC AGC TTT GCG
N W P E R F G F V L I S F A
GTC CAG TTC ACG CTC AAC CAC TTC TCC GGC GAC ACA TAC GTG
V Q F T L N H F S G D T Y V

FIGURE 10C

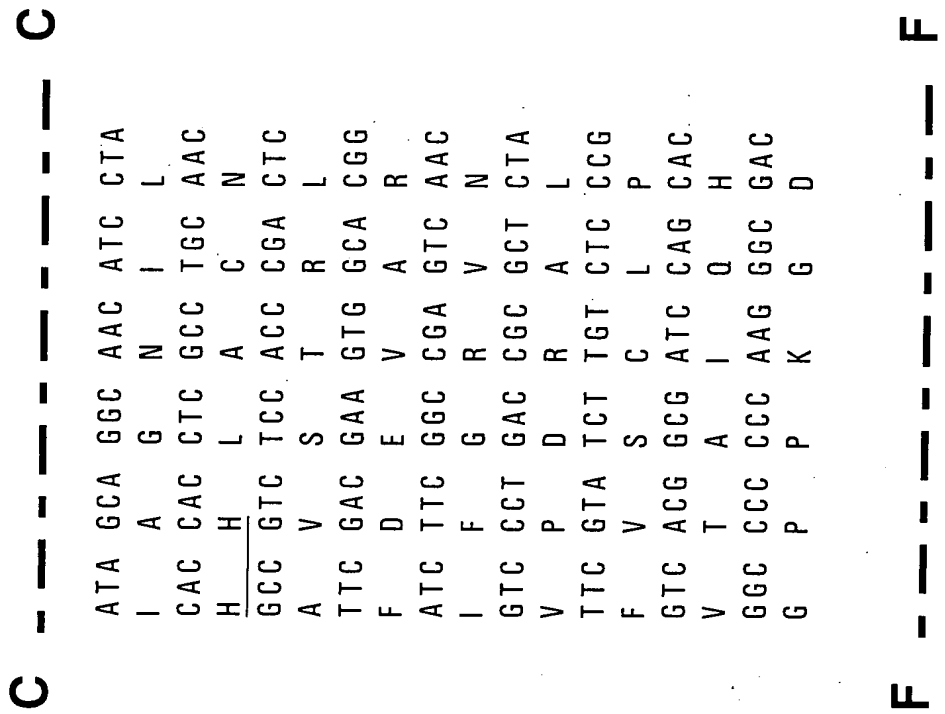

C
C
D
D
F
F
ATA GCA GGC AAC ATC CTA
I A G N I L
CAC CAC CTC GCC TGC AAC
H H L A C N
GCC GTC TCC ACC CGA CTC
A V S T R L
TTC GAC GAA GTG GCA CGG
F D E V A R
ATC TTC GGC CGA GTC AAC
I F G R V N
GTC CCT GAC CGC GCT CTA
V P D R A L
TTC GTA TCT TGT CTC CCG
F V S C L P
GTC ACG GCG ATC CAG CAC
V T A I Q H
GGC CCC CCC AAG GGC GAC
G P P K G D

FIGURE 10D

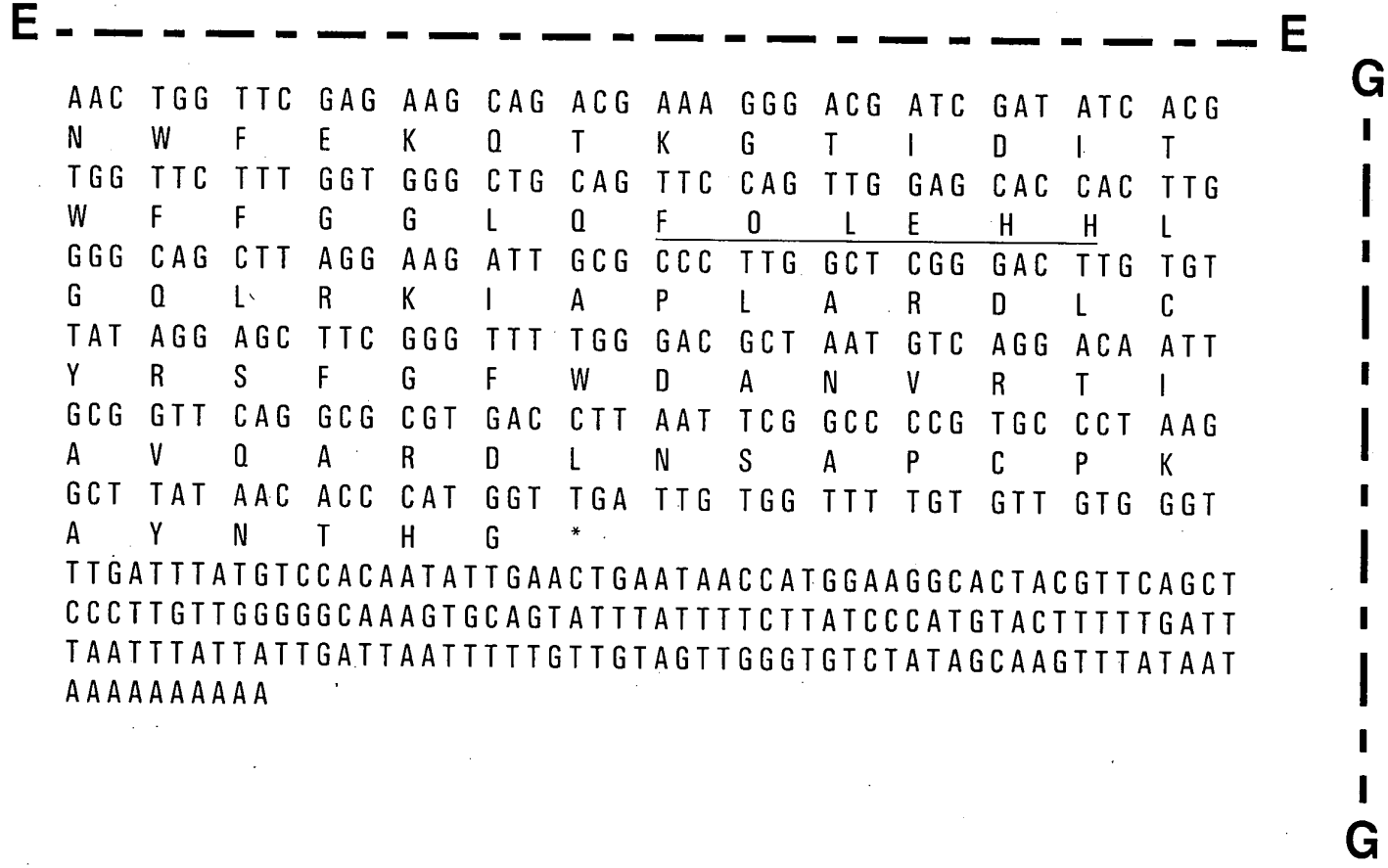

E
E
G
G
AAC TGG TTC GAG AAG CAG ACG AAA GGG ACG ATC GAT ATC ACG
N W F E K Q T K G T I D I T
TGG TTC TTT GGT GGG CTG CAG TTC CAG TTG GAG CAC CAC TTG
W F F G G L Q F Q L E H H L
GGG CAG CTT AGG AAG ATT GCG CCC TTG GCT CGG GAC TTG TGT
G Q L R K I A P L A R D L C
TAT AGG AGC TTC GGG TTT TGG GAC GCT AAT GTC AGG ACA ATT
Y R S F G F W D A N V R T I
GCG GTT CAG GCG CGT GAC CTT AAT TCG GCC CCG TGC CCT AAG
A V Q A R D L N S A P C P K
GCT TAT AAC ACC CAT GGT TGA TTG TGG TTT TGT GTT GTG GGT
A Y N T H G *
TTGATTTATGTCCACAATATTGAACTGAATAACCATGGAAGGCACTACGTTCAGCT
CCCTTGTTGGGGGCAAAGTGCAGTATTTATTTTCTTATCCCATGTACTTTTTGATT
TAATTTATTATTGATTAATTTTTGTTGTAGTTGGGTGTCTATAGCAAGTTTATAAT
AAAAAAAAAA

FIGURE 10E

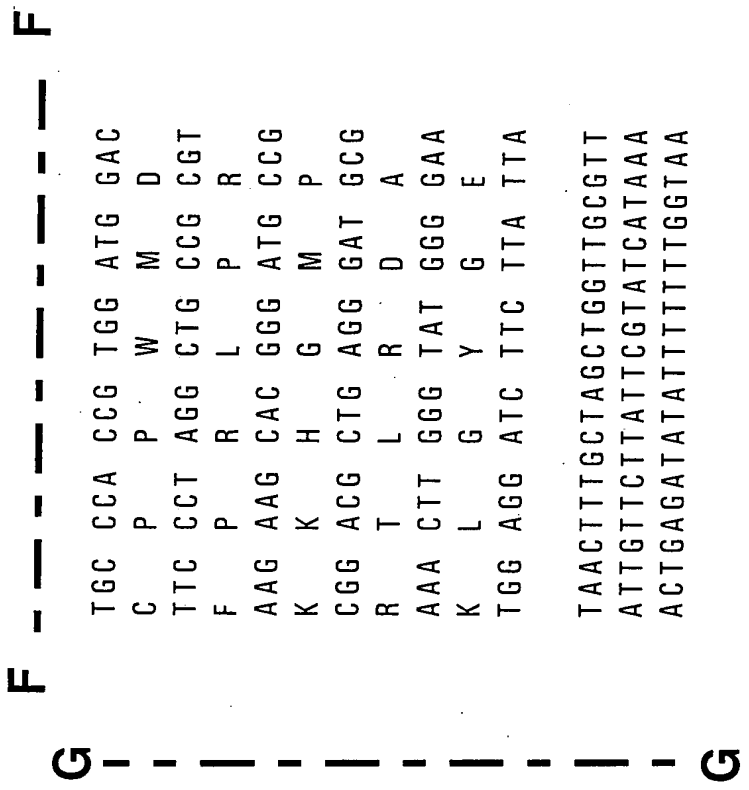

F
TGC CCA CCG TGG ATG GAC
C P P W M D
TTC CCT AGG CTG CCG CGT
F P R L P R
AAG AAG CAC GGG ATG CCG
K K H G M P
CGG ACG CTG AGG GAT GCG
R T L R D A
AAA CTT GGG TAT GGG GAA
K L G Y G E
TGG AGG ATC TTC TTA TTA
F
G
TAACTTTGCTAGCTGGTTGCGTT
ATTGTTCTTATTCGTATCATAAA
ACTGAGATATATTTTTTTGGTAA
G

FIGURE 10F

EP vs Bo Delta 6-desaturase Formatted Alignment

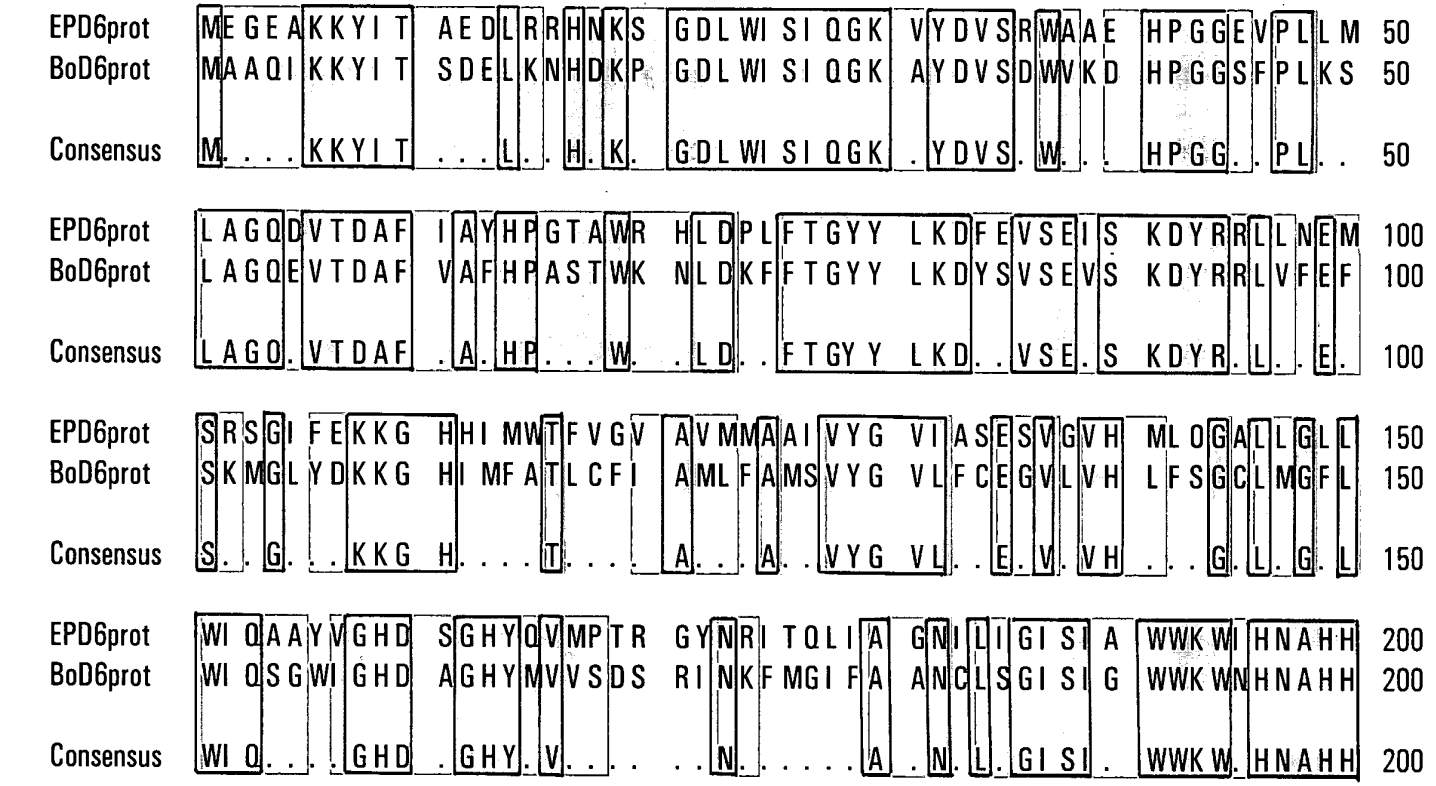


FIGURE 11A

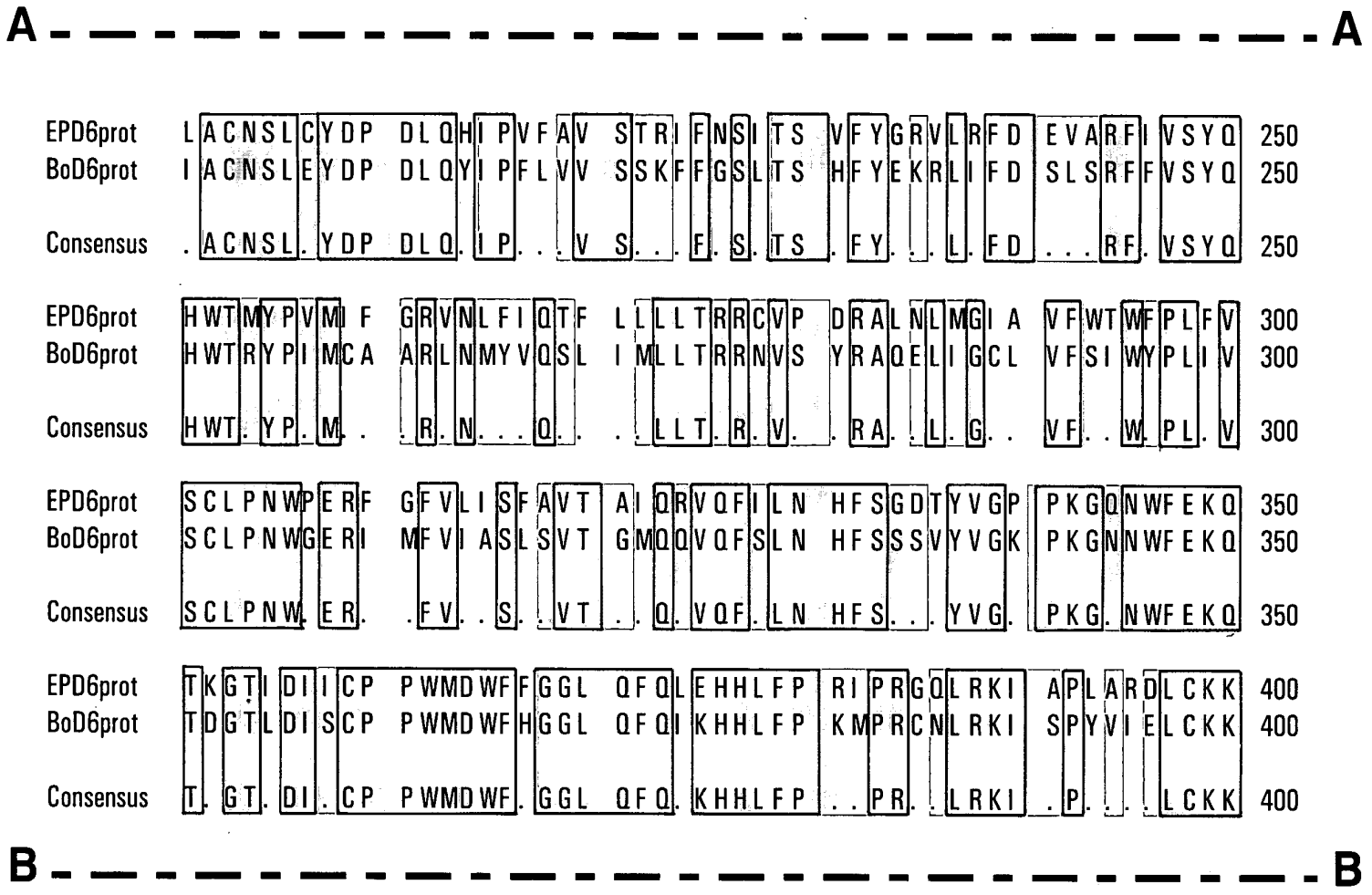

A
A
EPD6prot LACNSLCYDP DLQHIPVFAV STRIFNSITS VFYGRVLRFD EVARFIVSYQ 250
BoD6prot IACNSLEYDP DLQYIPFLVV SSKFFGSLTS HFYEKRLIFD SLSRFFVSYQ 250
Consensus .ACNSL.YDP DLQ.IP. . .V S. . .F. S. TS .FY. . .L. FD . . . RF. VSYQ 250
EPD6prot HWTMYPVMIF GRVNLFIQTF LLLLTRRCVP DRALNLMGIA VFWTWFPLFV 300
BoD6prot HWTRYPIMCA ARLNMYVQSL IMLLTRRNVS YRAQELIGCL VFSIWYPLIV 300
Consensus HWT. YP. M. . . R. N. . . Q. . . . LLT. R. V. . . RA. . L. G. . VF. . W. PL. V 300
EPD6prot SCLPNWPERF GFVLISFAVT AIQRVQFILN HFSGDTYVGP PKGQNWFEKQ 350
BoD6prot SCLPNWGERI MFVIASLSVT GMQQVQFSLN HFSSSVYVGK PKGNNWFEKQ 350
Consensus SCLPNW. ER. .FV. . S. . VT . . Q. VQF. LN HFS. . . YVG. PKG. NWFEKQ 350
EPD6prot TKGTIDIICP PWMDWFFGGL QFQLEHHLFP RIPRGQLRKI APLARDLCKK 400
BoD6prot TDGTLDISCP PWMDWFHGGL QFQIKHHLFP KMPRCNLRKI SPYVIELCKK 400
Consensus T. GT. DI. CP PWMDWF. GGL QFQ. KHHLFP . . PR. . LRKI . P. . . . LCKK 400
B
B

FIGURE 11B

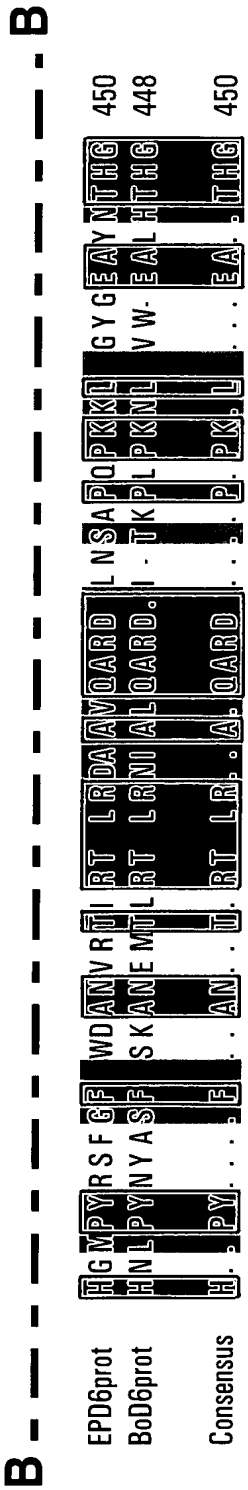
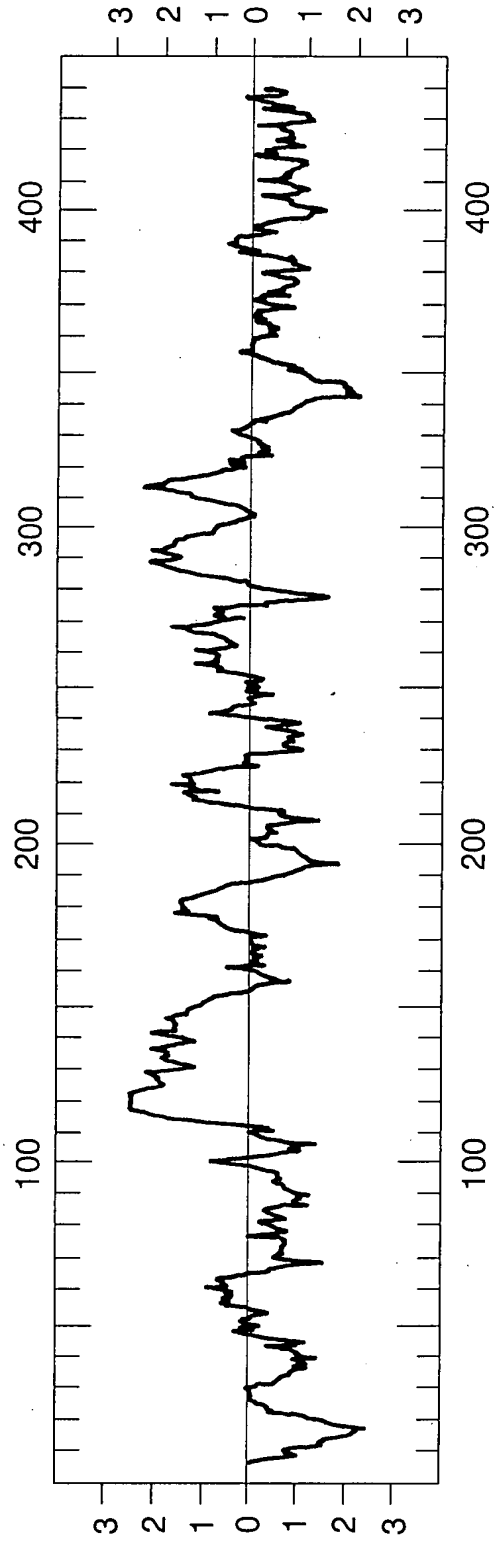
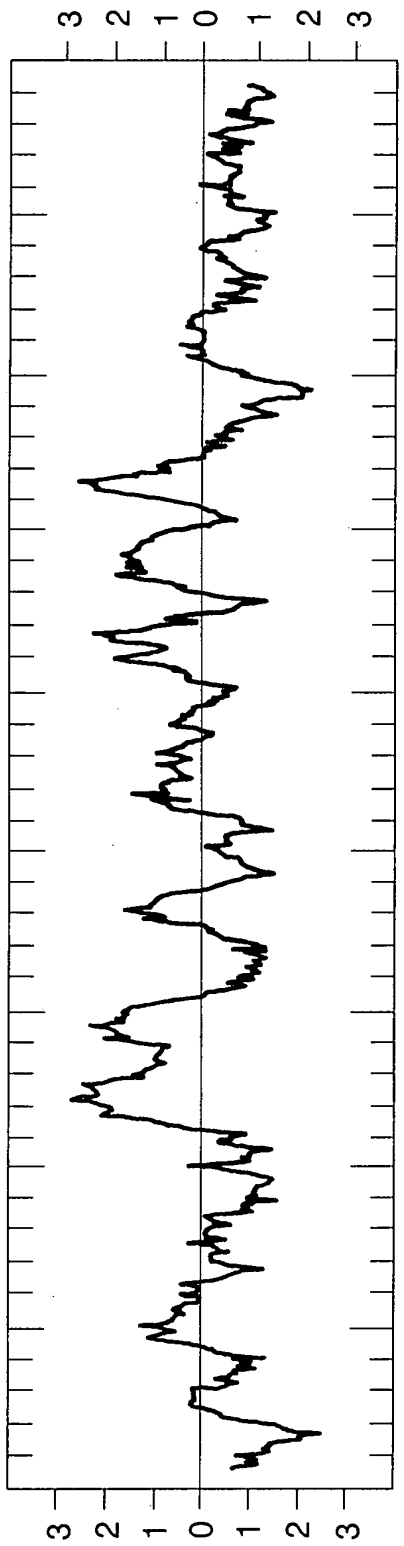


FIGURE 11C



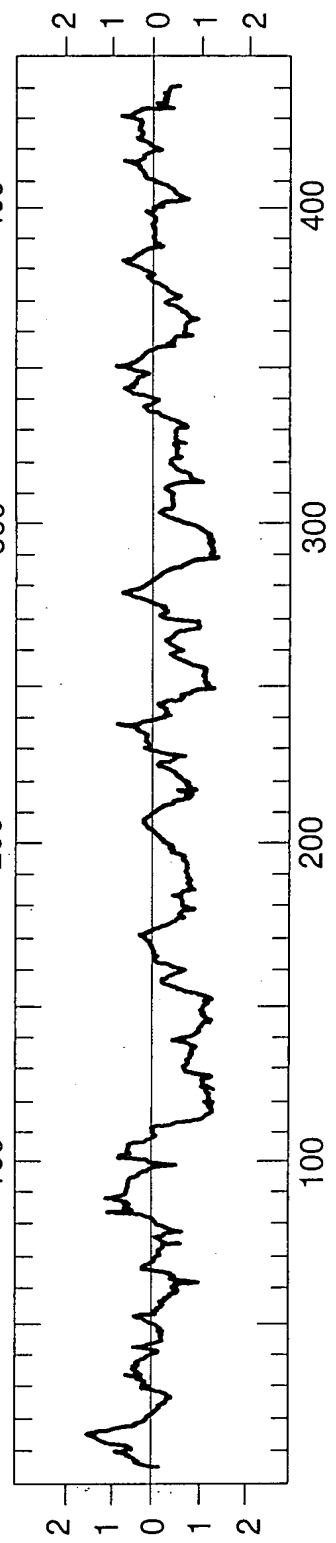
Borage Δ^6-Desaturase Kyte-Doolittle Hydrophobicity Plot

FIGURE 12A



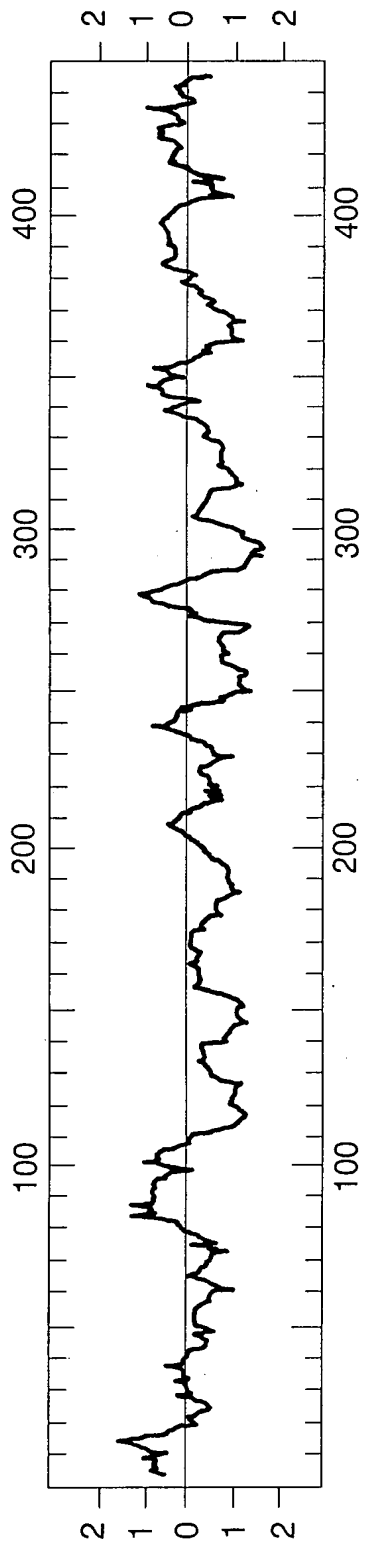
Evening Primrose Putative Δ^6-Desaturase Kyte-Doolittle Hydrophobicity Plot

FIGURE 12B



Borage Δ^6-Desaturase Hopwood Hydrophilicity Plot

FIGURE 13A



Evening Primrose Putative Δ^6-Desaturase Hopwood Hydrophilicity Plot

FIGURE 13B

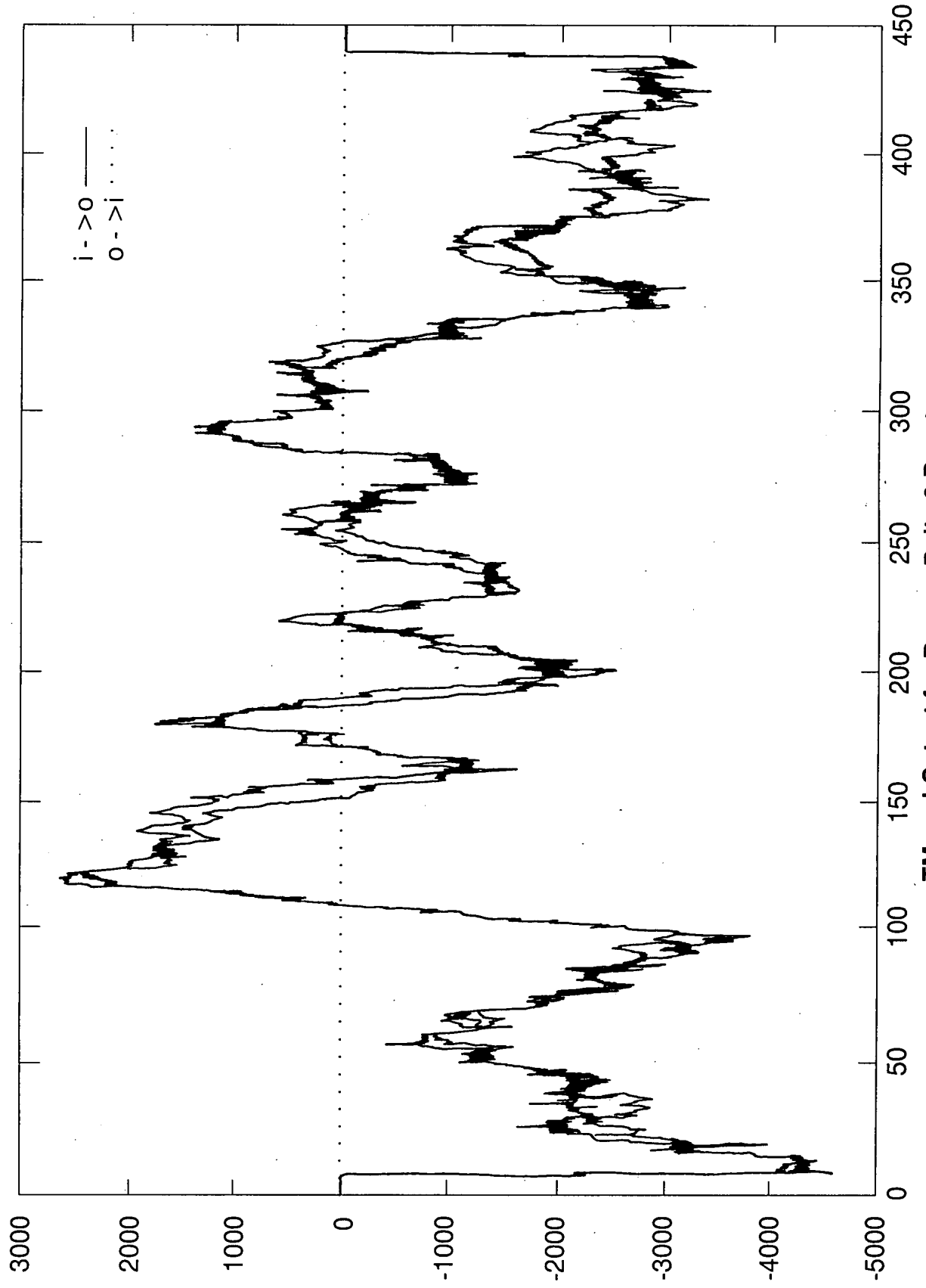

i - >o
o - >i
TMpred Output for Borage Delta 6-Desaturase
3000
2000
1000
0
-1000
-2000
-3000
-4000
-5000
0
50
100
150
200
250
300
350
400
450

FIGURE 14A

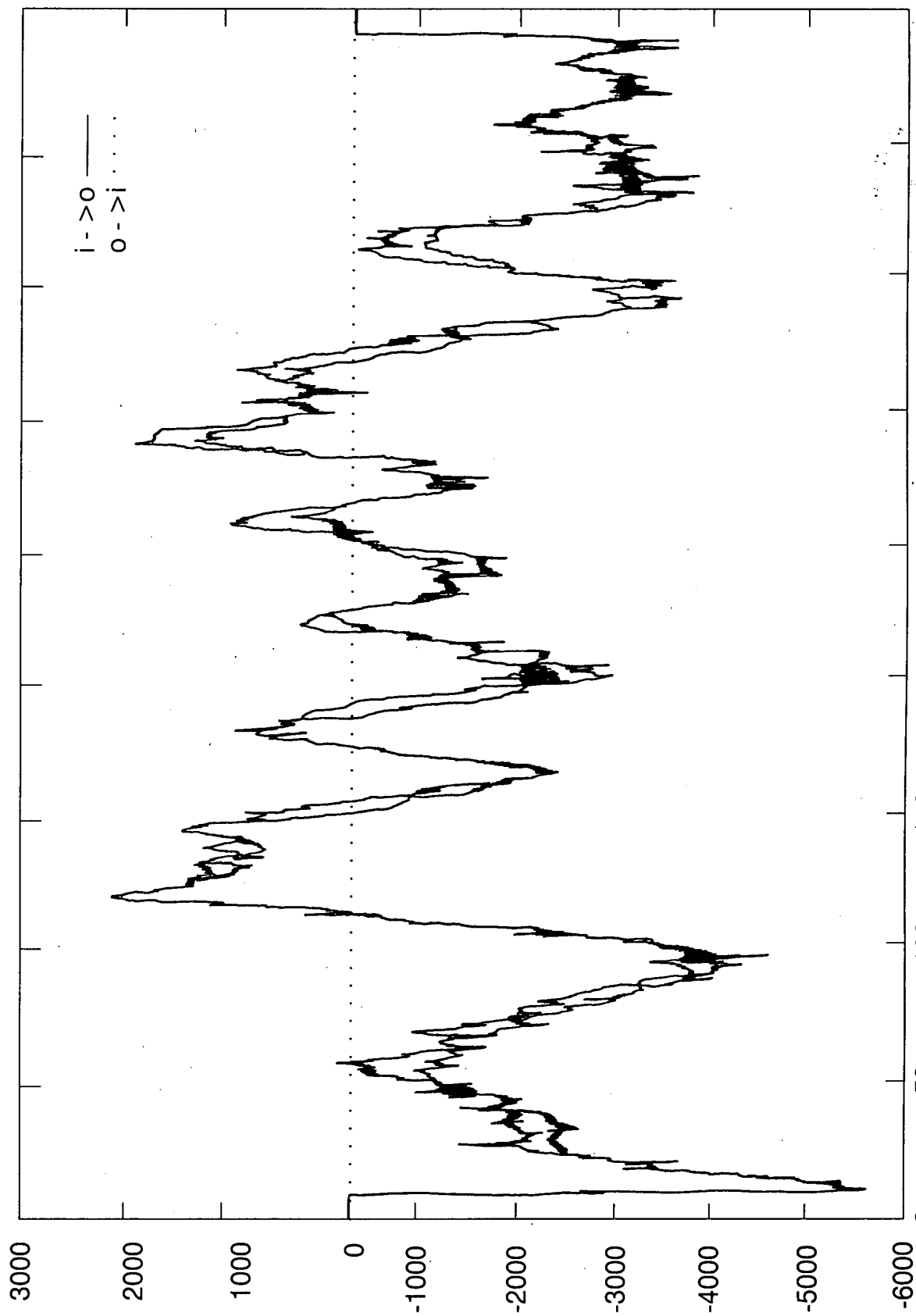

i - >o
o - >i
3000
2000
1000
0
-1000
-2000
-3000
-4000
-5000
-6000
0
50
100
150
200
250
300
350
400
450
TMpred Output for Evening Primrose Seq

FIGURE 14B